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SEQUENCE LISTING

<110> The University of Queensland (all states, except U.S.)
 Frazer, Ian Hector (U.S. only)

<120> A method for optimising gene expression

<130> 12178192/VPA

<140> Unassigned

<141> 2003-11-10

<150> USSN 60/425,163

<151> 2002-11-08

<160> 126

<170> PatentIn version 3.2

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<221> CDS

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Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu	
1 5 10 15	
ctg gat ggc gat gtg aat ggg cac aaa ttt tct gtc agc gga gag ggt	96
Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly	
20 25 30	
gaa ggt gat gcc aca tac gga aag ctc acc ctg aaa ttc atc tgc acc	144
Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr	
35 40 45	
act gga aag ctc cct gtg cca tgg cca aca ctg gtc act acc ttc tct	192
Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser	
50 55 60	
tat ggc gtg cag tgc ttt tcc aga tac cca gac cat atg aag cag cat	240
Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His	
65 70 75 80	
gac ttt ttc aag agc gcc atg ccc gag ggc tat gtg cag gag aga acc	288
Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr	
85 90 95	
atc ttt ttc aaa gat gac ggg aac tac aag acc cgc gct gaa gtc aag	336
Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys	
100 105 110	
ttc gaa ggt gac acc ctg gtg aat aga atc gag ctg aag ggc att gac	384

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
 115 120 125
 ttt aag gag gat gga aac att ctc ggc cac aag ctg gaa tac aac tat 432
 Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
 130 135 140
 aac tcc cac aat gtg tac atc atg gcc gac aag caa aag aat ggc atc 480
 Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
 145 150 155 160
 aag gtc aac ttc aag atc aga cac aac att gag gat gga tcc gtg cag 528
 Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
 165 170 175
 ctg gcc gac cat tat caa cag aac act cca atc ggc gac ggc cct gtg 576
 Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
 180 185 190
 ctc ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct aaa 624
 Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
 195 200 205
 gat ccc aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg acc 672
 Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
 210 215 220
 gct gct ggg atc aca cat ggc atg gac gag ctg tac aag tga 714
 Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

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 Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
 1 5 10 15

 Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
 20 25 30

 Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
 35 40 45

 Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser
 50 55 60

 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
 65 70 75 80

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
85 90 95

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
100 105 110

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
115 120 125

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
130 135 140

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
145 150 155 160

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
165 170 175

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
180 185 190

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
195 200 205

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
210 215 220

Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

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<222> (1) .. (18)

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Ala Ala Ala Ala Ala Ala

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 1 5

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 1 5

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 Arg Arg Arg Arg Arg Arg
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agg agg agg agg agg agg

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<213> Artificial Sequence

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<223> Arg (CGC) x6

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<221> CDS

<222> (1) .. (18)

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<223> Arg (CGC) x6

<400> 22

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1 5

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<400> 24

Asn Asn Asn Asn Asn Asn
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<400> 26

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<400> 28

Asp Asp Asp Asp Asp Asp
1 5

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1 5

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<220>
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Asp Asp Asp Asp Asp Asp
 1 5

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<221> CDS

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 Cys Cys Cys Cys Cys Cys
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<220>

<223> Cys (TGC)x6

<400> 32

Cys Cys Cys Cys Cys Cys
 1 5

<210> 33

<211> 18

<212> DNA

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<220>

<223> Cys (TGT)x6

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<221> CDS

<222> (1) .. (18)

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<223> Cys (TGT) x6

<400> 34

Cys Cys Cys Cys Cys Cys
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<210> 35

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<223> Gln(CAA) x6

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<221> CDS

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caa caa caa caa caa caa
 Gln Gln Gln Gln Gln Gln
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18

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<211> 6

<212> PRT

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<223> Gln(CAA) x6

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<210> 37

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<221> CDS

<222> (1) .. (18)

<400> 37

cag cag cag cag cag cag
 Gln Gln Gln Gln Gln Gln
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18

<210> 38
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<220>
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<400> 38

Gln Gln Gln Gln Gln Gln
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<210> 39
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gaa gaa gaa gaa gaa gaa
Glu Glu Glu Glu Glu Glu
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Glu Glu Glu Glu Glu Glu
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Glu Glu Glu Glu Glu Glu
1 5

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<400> 42

Glu Glu Glu Glu Glu Glu
1 5

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Gly Gly Gly Gly Gly Gly
1 5

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<210> 45
<211> 18
<212> DNA
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<223> Gly(GGG)x6

<400> 46

Gly Gly Gly Gly Gly Gly
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<210> 47

<211> 18

<212> DNA

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<223> Gly(GGC)x6

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<221> CDS

<222> (1) .. (18)

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Gly Gly Gly Gly Gly Gly
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<211> 6

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<223> Gly(GGC)x6

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Gly Gly Gly Gly Gly Gly
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<211> 18

<212> DNA

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<212> DNA
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His His His His His His
1 5

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His His His His His His
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<221> CDS

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<400> 53

cat cat cat cat cat cat

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His His His His His His

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<220>

<223> His (CAT)x6

<400> 54

His His His His His His

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5

<210> 55

<211> 18

<212> DNA

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<220>

<221> CDS

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<400> 55

atc atc atc atc atc atc

18

Ile Ile Ile Ile Ile Ile

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<212> PRT

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<223> Ile (ATC)x6

<400> 56

Ile Ile Ile Ile Ile Ile

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att att att att att att
Ile Ile Ile Ile Ile Ile
1 5

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<400> 58

Ile Ile Ile Ile Ile Ile
1 5

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ata ata ata ata ata ata
Ile Ile Ile Ile Ile Ile
1 5

18

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<211> 6
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Ile Ile Ile Ile Ile Ile
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ctc ctc ctc ctc ctc ctc
Leu Leu Leu Leu Leu Leu
1 5

18

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<220>
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Leu Leu Leu Leu Leu Leu
1 5

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<220>
<221> CDS
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ttg ttg ttg ttg ttg ttg
Leu Leu Leu Leu Leu Leu
1 5

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<220>

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Leu Leu Leu Leu Leu Leu

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5

<210> 65

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<221> CDS

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cta cta cta cta cta cta

18

Leu Leu Leu Leu Leu Leu

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<220>

<223> Leu(CTA)x6

<400> 66

Leu Leu Leu Leu Leu Leu

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<400> 67

ctg ctg ctg ctg ctg ctg

18

Leu Leu Leu Leu Leu Leu

1

5

<210> 68

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<220>
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<400> 68

Leu Leu Leu Leu Leu Leu
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<222> (1)..(18)

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tta tta tta tta tta tta
Leu Leu Leu Leu Leu Leu
1 5

18

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<212> PRT
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<220>
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<400> 70

Leu Leu Leu Leu Leu Leu
1 5

<210> 71
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<220>
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<220>
<221> CDS
<222> (1)..(18)

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ctt ctt ctt ctt ctt ctt
Leu Leu Leu Leu Leu Leu

18

1 5

<210> 72
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Leu(CTT)x6

<400> 72

Leu Leu Leu Leu Leu Leu
1 5

<210> 73
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<212> DNA
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<220>
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<220>
<221> CDS
<222> (1)..(18)

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aag aag aag aag aag aag
Lys Lys Lys Lys Lys Lys
1 5

18

<210> 74
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Lys(AAG)x6

<400> 74

Lys Lys Lys Lys Lys Lys
1 5

<210> 75
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Lys(AAA)x6

<220>
<221> CDS
<222> (1)..(18)

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aaa aaa aaa aaa aaa aaa
Lys Lys Lys Lys Lys Lys
1 5 18

<210> 76
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Lys (AAA)x6

<400> 76
Lys Lys Lys Lys Lys Lys
1 5

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<220>
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<222> (1) .. (18)

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ttt ttt ttt ttt ttt ttt
Phe Phe Phe Phe Phe Phe
1 5 18

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<212> PRT
<213> Artificial sequence

<220>
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<400> 78
Phe Phe Phe Phe Phe Phe
1 5

<210> 79
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<220>
<221> CDS
<222> (1)..(18)

<400> 79
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1 5

<210> 80
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<212> PRT
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<220>
<223> Phe(TTC)x6

<400> 80
Phe Phe Phe Phe Phe Phe
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<210> 81
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<220>
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<400> 81
ccc ccc ccc ccc ccc ccc 18
Pro Pro Pro Pro Pro Pro
1 5

<210> 82
<211> 6
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<220>
<223> Pro(CCC)x6

<400> 82
Pro Pro Pro Pro Pro Pro
1 5

<210> 83
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Pro (CCT) x6

<220>

<221> CDS

<222> (1) .. (18)

<400> 83

cct cct cct cct cct cct

18

Pro Pro Pro Pro Pro Pro

1

5

<210> 84

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Pro (CCT) x6

<400> 84

Pro Pro Pro Pro Pro Pro

1

5

<210> 85

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Pro (CCG) x6

<220>

<221> CDS

<222> (1) .. (18)

<400> 85

ccg ccg ccg ccg ccg ccg

18

Pro Pro Pro Pro Pro Pro

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<210> 86

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Pro (CCG) x6

<400> 86

Pro Pro Pro Pro Pro Pro

1

5

<210> 87
 <211> 18
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Pro(CCA)x6

<220>
 <221> CDS
 <222> (1)..(18)

<400> 87
 cca cca cca cca cca cca
 Pro Pro Pro Pro Pro Pro
 1 5

18

<210> 88
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Pro(CCA)x6

<400> 88

Pro Pro Pro Pro Pro Pro
 1 5

<210> 89
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Ser(AGC)x6

<220>
 <221> CDS
 <222> (1)..(18)

<400> 89
 agc agc agc agc agc agc
 Ser Ser Ser Ser Ser Ser
 1 5

18

<210> 90
 <211> 6
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<220>
 <223> Ser(AGC)x6

<400> 90

Ser Ser Ser Ser Ser Ser
1 5

<210> 91
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Ser(TCT)x6

<220>
<221> CDS
<222> (1)..(18)

<400> 91
tct tct tct tct tct tct
Ser Ser Ser Ser Ser Ser
1 5

18

<210> 92
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Ser(TCT)x6

<400> 92

Ser Ser Ser Ser Ser Ser
1 5

<210> 93
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Ser(AGT)x6

<220>
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<222> (1)..(18)

<400> 93
agt agt agt agt agt agt
Ser Ser Ser Ser Ser Ser
1 5

18

<210> 94
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Ser(AGT)x6

<400> 94

Ser Ser Ser Ser Ser Ser
1 5

<210> 95

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Ser(TCG)x6

<220>

<221> CDS

<222> (1)..(18)

<400> 95

tcg tcg tcg tcg tcg tcg
Ser Ser Ser Ser Ser Ser
1 5

18

<210> 96

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Ser(TCG)x6

<400> 96

Ser Ser Ser Ser Ser Ser
1 5

<210> 97

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Ser(TCA)x6

<220>

<221> CDS

<222> (1)..(18)

<400> 97

tca tca tca tca tca tca
Ser Ser Ser Ser Ser Ser
1 5

18

<210> 98

<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Ser(TCA)x6

<400> 98

Ser Ser Ser Ser Ser Ser
1 5

<210> 99
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Ser(TCC)x6

<220>
<221> CDS
<222> (1)..(18)

<400> 99
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Ser Ser Ser Ser Ser Ser
1 5

18

<210> 100
<211> 6
<212> PRT
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<220>
<223> Ser(TCC)x6

<400> 100

Ser Ser Ser Ser Ser Ser
1 5

<210> 101
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Thr(ACA)x6

<220>
<221> CDS
<222> (1)..(18)

<400> 101
aca aca aca aca aca aca
Thr Thr Thr Thr Thr Thr
1 5

18

<210> 102
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Thr(ACA)x6

<400> 102

Thr Thr Thr Thr Thr Thr
1 5

<210> 103
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Thr(ACG)x6

<220>
<221> CDS
<222> (1) .. (18)

<400> 103
acg acg acg acg acg acg
Thr Thr Thr Thr Thr Thr
1 5

18

<210> 104
<211> 6
<212> PRT
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<220>
<223> Thr(ACG)x6

<400> 104

Thr Thr Thr Thr Thr Thr
1 5

<210> 105
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Thr(ACT)x6

<220>
<221> CDS
<222> (1) .. (18)

<400> 105
act act act act act act
Thr Thr Thr Thr Thr Thr
1 5

18

<210> 106
<211> 6
<212> PRT
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<220>
<223> Thr(ACI)x6

<400> 106

Thr Thr Thr Thr Thr Thr
1 5

<210> 107
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Thr(ACC)x6

<220>
<221> CDS
<222> (1)..(18)

<400> 107
acc acc acc acc acc acc
Thr Thr Thr Thr Thr Thr
1 5

18

<210> 108
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Thr(ACC)x6

<400> 108

Thr Thr Thr Thr Thr Thr
1 5

<210> 109
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Tyr(TAC)x6

<220>
<221> CDS
<222> (1)..(18)

<400> 109
tac tac tac tac tac tac
Tyr Tyr Tyr Tyr Tyr Tyr
1 5

18

<210> 110
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Tyr(TAC)x6

<400> 110

Tyr Tyr Tyr Tyr Tyr Tyr
1 5

<210> 111
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Tyr(TAT)x6

<220>
<221> CDS
<222> (1)..(18)

<400> 111
tat tat tat tat tat tat
Tyr Tyr Tyr Tyr Tyr Tyr
1 5

18

<210> 112
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Tyr(TAT)x6

<400> 112

Tyr Tyr Tyr Tyr Tyr Tyr
1 5

<210> 113
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Val (GTG)x6

<220>

<221> CDS

<222> (1) .. (18)

<400> 113

gtg gtg gtg gtg gtg gtg

18

Val Val Val Val Val Val

1

5

<210> 114

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Val (GTG)x6

<400> 114

Val Val Val Val Val Val

1

5

<210> 115

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Val (GTT)x6

<220>

<221> CDS

<222> (1) .. (18)

<400> 115

gtt gtt gtt gtt gtt gtt

18

Val Val Val Val Val Val

1

5

<210> 116

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Val (GTT)x6

<400> 116

Val Val Val Val Val Val

1

5

<210> 117

<211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Val (GTC)x6

<220>
 <221> CDS
 <222> (1)..(18)

<400> 117
 gtc gtc gtc gtc gtc gtc
 Val Val Val Val Val Val
 1 5

18

<210> 118
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Val (GTC)x6

<400> 118

Val Val Val Val Val Val
 1 5

<210> 119
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Val (GTA)x6

<220>
 <221> CDS
 <222> (1)..(18)

<400> 119
 gta gta gta gta gta gta
 Val Val Val Val Val Val
 1 5

18

<210> 120
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Val (GTA)x6

<400> 120

Val Val Val Val Val Val

1

5

<210> 121
 <211> 2583
 <212> DNA
 <213> Mouse

<220>
 <221> CDS
 <222> (1) .. (2166)

<400> 121
 gaa ctt cgg gac gag caa act ccg ggc cac agg aag aac cca tcg aac 48
 Glu Leu Arg Asp Glu Gln Thr Pro Gly His Arg Lys Asn Pro Ser Asn
 1 5 10 15

caa agc agc tta gaa tct gac tcc aat tac ccc tcc att tcc act tcc 96
 Gln Ser Ser Leu Glu Ser Asp Ser Asn Tyr Pro Ser Ile Ser Thr Ser
 20 25 30

gaa atc gga gac act gag gat gcc ctt cag cag gtg gag gag att ggc 144
 Glu Ile Gly Asp Thr Glu Asp Ala Leu Gln Gln Val Glu Glu Ile Gly
 35 40 45

ata gag aag gca gcc atg gac atg acc gtc ttc ctg aag ctg cag aag 192
 Ile Glu Lys Ala Ala Met Asp Met Thr Val Phe Leu Lys Leu Gln Lys
 50 55 60

aga gtg cgc gaa ctt gag cag gag agg aag aag ctg cag gcg cag cta 240
 Arg Val Arg Glu Leu Glu Gln Glu Arg Lys Lys Leu Gln Ala Gln Leu
 65 70 75 80

gaa aag gga cag cag gac agc aag aaa ggg cag gta gaa caa cag aac 288
 Glu Lys Gly Gln Gln Asp Ser Lys Lys Gly Gln Val Glu Gln Gln Asn
 85 90 95

aat ggc tta gat gtg gac cag gac gca gat ata gcc tac aat agt ctg 336
 Asn Gly Leu Asp Val Asp Gln Asp Ala Asp Ile Ala Tyr Asn Ser Leu
 100 105 110

aag aga cag gag ctt gag tca gag aac aag aag ctg aag aat gac ctg 384
 Lys Arg Gln Glu Leu Glu Ser Glu Asn Lys Lys Leu Lys Asn Asp Leu
 115 120 125

aat gag ctg agg aac ggt gtc gct gac caa gcc atg cag gat aac tcc 432
 Asn Glu Leu Arg Asn Gly Val Ala Asp Gln Ala Met Gln Asp Asn Ser
 130 135 140

acc cac agc tcc cca gac agc tac agc ctc cta ctg aac cag ctc aag 480
 Thr His Ser Ser Pro Asp Ser Tyr Ser Leu Leu Leu Asn Gln Leu Lys
 145 150 155 160

ctg gcc aat gag gag ctc gag gtc cgc aaa gag gag gcg ctg atc ctc 528
 Leu Ala Asn Glu Glu Leu Glu Val Arg Lys Glu Glu Ala Leu Ile Leu
 165 170 175

agg acc cag atc atg aat gcc gac cag cgc cgc ctg tct ggc aag aac 576
 Arg Thr Gln Ile Met Asn Ala Asp Gln Arg Arg Leu Ser Gly Lys Asn
 180 185 190

atg gag ccg aac atc aat gcc aga aca agt tgg ccc aac agt gag aag Met Glu Pro Asn Ile Asn Ala Arg Thr Ser Trp Pro Asn Ser Glu Lys 195 200 205	624
cac gtg gac cag gaa gac gcc att gag gcc tat cac ggg gtc tgc cag His Val Asp Gln Glu Asp Ala Ile Glu Ala Tyr His Gly Val Cys Gln 210 215 220	672
aca aac agg ttg ctg gag gcc cag ctg cag gcc cag agc ctg gag cat Thr Asn Arg Leu Leu Glu Ala Gln Leu Gln Ala Gln Ser Leu Glu His 225 230 235 240	720
gag gag gag gtg gaa cat ctc aag gcc cag gtg gaa gcc ctg aaa gag Glu Glu Glu Val Glu His Leu Lys Ala Gln Val Glu Ala Leu Lys Glu 245 250 255	768
gag atg gac aaa cag cag cag acc ttc tgc cag acc ctg ctg ctc tcc Glu Met Asp Lys Gln Gln Gln Thr Phe Cys Gln Thr Leu Leu Leu Ser 260 265 270	816
cca gag gcc cag gta gaa ttt ggt gtc cag cag gag ata tcc cgg ctg Pro Glu Ala Gln Val Glu Phe Gly Val Gln Gln Glu Ile Ser Arg Leu 275 280 285	864
acc aat gag aac ctg gat ttt aag gaa ttg gtg gaa aag ctg gag aag Thr Asn Glu Asn Leu Asp Phe Lys Glu Leu Val Glu Lys Leu Glu Lys 290 295 300	912
aat gag agg aag ctg aag aag cag ctg aag att tac atg aag aag gtc Asn Glu Arg Lys Leu Lys Lys Gln Leu Lys Ile Tyr Met Lys Lys Val 305 310 315 320	960
cag gac tta gaa gct gcc cag gcg ttg gca cag agt gac agg agg cac Gln Asp Leu Glu Ala Ala Gln Ala Leu Gln Ser Asp Arg Arg His 325 330 335	1008
cat gaa ctc aca aga cag gtc aca gtc caa cga aaa gag aag gac ttc His Glu Leu Thr Arg Gln Val Thr Val Gln Arg Lys Glu Lys Asp Phe 340 345 350	1056
caa ggc atg ctg gag tac cac aaa gag gtc gaa gcc ctc ctc atc cgg Gln Gly Met Leu Glu Tyr His Lys Glu Val Glu Ala Leu Leu Ile Arg 355 360 365	1104
aac ctg gtg aca gac ctg aag cct cag atg ctg ctg ggc acc gtg ccc Asn Leu Val Thr Asp Leu Lys Pro Gln Met Leu Leu Gly Thr Val Pro 370 375 380	1152
tgt ctg cct gca tac ata ctc tat atg tgc atc agg cac gcg gat tac Cys Leu Pro Ala Tyr Ile Leu Tyr Met Cys Ile Arg His Ala Asp Tyr 385 390 395 400	1200
acc aac gat gac ctc aag gtg cac tcg ttg ctg agc tcc acc atc aac Thr Asn Asp Asp Leu Lys Val His Ser Leu Leu Ser Ser Thr Ile Asn 405 410 415	1248
ggc att aag aaa gtc ctc aag aag cac aat gac gac ttt gag atg acg Gly Ile Lys Lys Val Leu Lys Lys His Asn Asp Asp Phe Glu Met Thr 420 425 430	1296
tca ttc tgg tta tcc aac acc tgc cgc ttc ctt cac tgt ctg aag caa Ser Phe Trp Leu Ser Asn Thr Cys Arg Phe Leu His Cys Leu Lys Gln	1344

435	440	445	
tac agt ggt gat gag ggt ttc atg aca cag aac atc gcg aag cag aat Tyr Ser Gly Asp Glu Gly Phe Met Thr Gln Asn Ile Ala Lys Gln Asn 450 455 460			1392
gag cac tgt ctc aag aac ttt gac ctc act gaa tac cgc cag gta cta Glu His Cys Leu Lys Asn Phe Asp Leu Thr Glu Tyr Arg Gln Val Leu 465 470 475 480			1440
agc gac ctt tcc att cag atc tat cag cag ctc att aaa atg ccc gag Ser Asp Leu Ser Ile Gln Ile Tyr Gln Gln Leu Ile Lys Met Pro Glu 485 490 495			1488
ggc ttg cta cag cct atg ata gtt tct gcc atg ttg gaa aat gag agt Gly Leu Leu Gln Pro Met Ile Val Ser Ala Met Leu Glu Asn Glu Ser 500 505 510			1536
atc cag ggg ctg tct ggt gtg aga cca act ggt tac cgg aag cgc tcc Ile Gln Gly Leu Ser Gly Val Arg Pro Thr Gly Tyr Arg Lys Arg Ser 515 520 525			1584
tcc agc atg gtg gat gga gag aat tct ttc cat aca gtc ctg tgt gac Ser Ser Met Val Asp Gly Glu Asn Ser Phe His Thr Val Leu Cys Asp 530 535 540			1632
cag ggc ctg gac ccc gag att atc ctg cag gtg ttc aaa cag ctc ttc Gln Gly Leu Asp Pro Glu Ile Ile Leu Gln Val Phe Lys Gln Leu Phe 545 550 555 560			1680
tac atg atc aat gct gtg act ctt aac aac cta ctc ctg cgg aaa gac Tyr Met Ile Asn Ala Val Thr Leu Asn Asn Leu Leu Leu Arg Lys Asp 565 570 575			1728
gcc tgc tcc tgg agc aca ggc atg caa ctc agg tac aac ata agt caa Ala Cys Ser Trp Ser Thr Gly Met Gln Leu Arg Tyr Asn Ile Ser Gln 580 585 590			1776
ctg gaa gag tgg ctt cgg ggc aaa aac ctt cac cag agt gga gca gtt Leu Glu Glu Trp Leu Arg Gly Lys Asn Leu His Gln Ser Gly Ala Val 595 600 605			1824
cag acc atg gag ccc ctg atc cag gca gcc cag ctc ctc cag ctg aag Gln Thr Met Glu Pro Leu Ile Gln Ala Ala Gln Leu Leu Gln Leu Lys 610 615 620			1872
aag aaa acc cac gag gat gct gag gcc atc tgc tct ctg tgc acc tcc Lys Lys Thr His Glu Asp Ala Glu Ala Ile Cys Ser Leu Cys Thr Ser 625 630 635 640			1920
ctc agc acc cag cag att gtc aaa att tta aac ctc tac act ccc ttg Leu Ser Thr Gln Gln Ile Val Lys Ile Leu Asn Leu Tyr Thr Pro Leu 645 650 655			1968
aat gaa ttt gag gaa cgg gtc aca gtg tcc ttc atc aga aca atc cag Asn Glu Phe Glu Glu Arg Val Thr Val Ser Phe Ile Arg Thr Ile Gln 660 665 670			2016
gct cag cta caa gag agg aat gac cct cag cag ctc ctg ctg gac tcc Ala Gln Leu Gln Glu Arg Asn Asp Pro Gln Gln Leu Leu Leu Asp Ser 675 680 685			2064

aag cac gtg ttc cca gtt ctg ttt cca tat aac cca tct gct ctg acc 2112
 Lys His Val Phe Pro Val Leu Phe Pro Tyr Asn Pro Ser Ala Leu Thr
 690 695 700

atg gac tcg atc cac atc ccg gcc tgt ctc aac ctg gag ttt ctc aat 2160
 Met Asp Ser Ile His Ile Pro Ala Cys Leu Asn Leu Glu Phe Leu Asn
 705 710 715 720

gaa gtc tgaggatgcg tgtttccgag gcgagcgaga aggaagcatg tgctgtcagc 2216
 Glu Val

cgagagaatg ctaggtgtgt taaatattcc agcgtagatc aaaccatggt agagactggc 2276

gggacgacag aactaaacag cgggggtgcac agttgtcgcc aatgctgctc agaaaacacc 2336

cggaagtgga tttgttaaag ctgtgctttc aggttaaacc aagacacgtc agaacgaaca 2396

gccactctgc agctccagtc gccatataaa aatgccagtt ctacagagtg gaagtgccta 2456

gctttgatct ttgtatatat cttgagaatg ttcaaactga gataatatta aaaacacatg 2516

acgtaaattg cctttgtggg tctttcaaga aatgatggga ctaataacca taagattgac 2576

aggaatt 2583

<210> 122

<211> 722

<212> PRT

<213> Mouse

<400> 122

Glu Leu Arg Asp Glu Gln Thr Pro Gly His Arg Lys Asn Pro Ser Asn
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Gln Ser Ser Leu Glu Ser Asp Ser Asn Tyr Pro Ser Ile Ser Thr Ser
 20 25 30

Glu Ile Gly Asp Thr Glu Asp Ala Leu Gln Gln Val Glu Glu Ile Gly
 35 40 45

Ile Glu Lys Ala Ala Met Asp Met Thr Val Phe Leu Lys Leu Gln Lys
 50 55 60

Arg Val Arg Glu Leu Glu Gln Glu Arg Lys Lys Leu Gln Ala Gln Leu
 65 70 75 80

Glu Lys Gly Gln Gln Asp Ser Lys Lys Gly Gln Val Glu Gln Gln Asn
 85 90 95

Asn Gly Leu Asp Val Asp Gln Asp Ala Asp Ile Ala Tyr Asn Ser Leu
 100 105 110

Lys Arg Gln Glu Leu Glu Ser Glu Asn Lys Lys Leu Lys Asn Asp Leu
 115 120 125

Asn Glu Leu Arg Asn Gly Val Ala Asp Gln Ala Met Gln Asp Asn Ser
 130 135 140

Thr His Ser Ser Pro Asp Ser Tyr Ser Leu Leu Leu Asn Gln Leu Lys
 145 150 155 160

Leu Ala Asn Glu Glu Leu Glu Val Arg Lys Glu Glu Ala Leu Ile Leu
 165 170 175

Arg Thr Gln Ile Met Asn Ala Asp Gln Arg Arg Leu Ser Gly Lys Asn
 180 185 190

Met Glu Pro Asn Ile Asn Ala Arg Thr Ser Trp Pro Asn Ser Glu Lys
 195 200 205

His Val Asp Gln Glu Asp Ala Ile Glu Ala Tyr His Gly Val Cys Gln
 210 215 220

Thr Asn Arg Leu Leu Glu Ala Gln Leu Gln Ala Gln Ser Leu Glu His
 225 230 235 240

Glu Glu Glu Val Glu His Leu Lys Ala Gln Val Glu Ala Leu Lys Glu
 245 250 255

Glu Met Asp Lys Gln Gln Gln Thr Phe Cys Gln Thr Leu Leu Leu Ser
 260 265 270

Pro Glu Ala Gln Val Glu Phe Gly Val Gln Gln Glu Ile Ser Arg Leu
 275 280 285

Thr Asn Glu Asn Leu Asp Phe Lys Glu Leu Val Glu Lys Leu Glu Lys
 290 295 300

Asn Glu Arg Lys Leu Lys Lys Gln Leu Lys Ile Tyr Met Lys Lys Val
 305 310 315 320

Gln Asp Leu Glu Ala Ala Gln Ala Leu Ala Gln Ser Asp Arg Arg His
 325 330 335

His Glu Leu Thr Arg Gln Val Thr Val Gln Arg Lys Glu Lys Asp Phe
 340 345 350

Gln Gly Met Leu Glu Tyr His Lys Glu Val Glu Ala Leu Leu Ile Arg
 355 360 365

Asn Leu Val Thr Asp Leu Lys Pro Gln Met Leu Leu Gly Thr Val Pro
 370 375 380

Cys Leu Pro Ala Tyr Ile Leu Tyr Met Cys Ile Arg His Ala Asp Tyr
 385 390 395 400

Thr Asn Asp Asp Leu Lys Val His Ser Leu Leu Ser Ser Thr Ile Asn
 405 410 415

Gly Ile Lys Lys Val Leu Lys Lys His Asn Asp Asp Phe Glu Met Thr
 420 425 430

Ser Phe Trp Leu Ser Asn Thr Cys Arg Phe Leu His Cys Leu Lys Gln
 435 440 445

Tyr Ser Gly Asp Glu Gly Phe Met Thr Gln Asn Ile Ala Lys Gln Asn
 450 455 460

Glu His Cys Leu Lys Asn Phe Asp Leu Thr Glu Tyr Arg Gln Val Leu
 465 470 475 480

Ser Asp Leu Ser Ile Gln Ile Tyr Gln Gln Leu Ile Lys Met Pro Glu
 485 490 495

Gly Leu Leu Gln Pro Met Ile Val Ser Ala Met Leu Glu Asn Glu Ser
 500 505 510

Ile Gln Gly Leu Ser Gly Val Arg Pro Thr Gly Tyr Arg Lys Arg Ser
 515 520 525

Ser Ser Met Val Asp Gly Glu Asn Ser Phe His Thr Val Leu Cys Asp
 530 535 540

Gln Gly Leu Asp Pro Glu Ile Ile Leu Gln Val Phe Lys Gln Leu Phe
 545 550 555 560

Tyr Met Ile Asn Ala Val Thr Leu Asn Asn Leu Leu Leu Arg Lys Asp
 565 570 575

Ala Cys Ser Trp Ser Thr Gly Met Gln Leu Arg Tyr Asn Ile Ser Gln
 580 585 590

Leu Glu Glu Trp Leu Arg Gly Lys Asn Leu His Gln Ser Gly Ala Val
 595 600 605

Gln Thr Met Glu Pro Leu Ile Gln Ala Ala Gln Leu Leu Gln Leu Lys
 610 615 620

Lys Lys Thr His Glu Asp Ala Glu Ala Ile Cys Ser Leu Cys Thr Ser
 625 630 635 640

Leu Ser Thr Gln Gln Ile Val Lys Ile Leu Asn Leu Tyr Thr Pro Leu
 645 650 655

Asn Glu Phe Glu Glu Arg Val Thr Val Ser Phe Ile Arg Thr Ile Gln
 660 665 670

Ala Gln Leu Gln Glu Arg Asn Asp Pro Gln Gln Leu Leu Leu Asp Ser
 675 680 685

Lys His Val Phe Pro Val Leu Phe Pro Tyr Asn Pro Ser Ala Leu Thr
 690 695 700

Met Asp Ser Ile His Ile Pro Ala Cys Leu Asn Leu Glu Phe Leu Asn
 705 710 715 720

Glu Val

<210> 123
 <211> 549
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BAR gene

<220>
 <221> CDS
 <222> (1)..(549)

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 1 5 10 15
 atg ccg gcg gtc tgc acc atc gtc aac cac tac atc gag aca agc acg 96
 Met Pro Ala Val Cys Thr Ile Val Asn His Tyr Ile Glu Thr Ser Thr
 20 25 30
 gtc aac ttc cgt acc gag ccg cag gaa ccg cag gag tgg acg gac gac 144
 Val Asn Phe Arg Thr Glu Pro Gln Glu Pro Gln Glu Trp Thr Asp Asp
 35 40 45
 ctc gtc cgt ctg cgg gag cgc tat ccc tgg ctc gtc gcc gag gtg gac 192
 Leu Val Arg Leu Arg Glu Arg Tyr Pro Trp Leu Val Ala Glu Val Asp
 50 55 60

ggc gag gtc gcc ggc atc gcc tac gcg ggc ccc tgg aag gca cgc aac 240
 Gly Glu Val Ala Gly Ile Ala Tyr Ala Gly Pro Trp Lys Ala Arg Asn
 65 70 75 80
 gcc tac gac tgg acg gcc gag tcg acc gtg tac gtc tcc ccc cgc cac 288
 Ala Tyr Asp Trp Thr Ala Glu Ser Thr Val Tyr Val Ser Pro Arg His
 85 90 95
 cag cgg acg gga ctg ggc tcc acg ctc tac acc cac ctg ctg aag tcc 336
 Gln Arg Thr Gly Leu Gly Ser Thr Leu Tyr Thr His Leu Leu Lys Ser
 100 105 110
 ctg gag gca cag ggc ttc aag agc gtg gtc gct gtc atc ggg ctg ccc 384
 Leu Glu Ala Gln Gly Phe Lys Ser Val Val Ala Val Ile Gly Leu Pro
 115 120 125
 aac gac ccg agc gtg cgc atg cac gag gcg ctc gga tat gcc ccc cgc 432
 Asn Asp Pro Ser Val Arg Met His Glu Ala Leu Gly Tyr Ala Pro Arg
 130 135 140
 ggc atg ctg cgg gcg gcc ggc ttc aag cac ggg aac tgg cat gac gtg 480
 Gly Met Leu Arg Ala Ala Gly Phe Lys His Gly Asn Trp His Asp Val
 145 150 155 160
 ggt ttc tgg cag ctg gac ttc agc ctg ccg gtg ccg ccc cgt ccg gtc 528
 Gly Phe Trp Gln Leu Asp Phe Ser Leu Pro Val Pro Pro Arg Pro Val
 165 170 175
 ctg ccc gtc acc gaa atc tga 549
 Leu Pro Val Thr Glu Ile
 180

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<400> 124

Ser Pro Glu Arg Arg Pro Ala Asp Ile Arg Arg Ala Thr Glu Ala Asp
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Met Pro Ala Val Cys Thr Ile Val Asn His Tyr Ile Glu Thr Ser Thr
 20 25 30

Val Asn Phe Arg Thr Glu Pro Gln Glu Pro Gln Glu Trp Thr Asp Asp
 35 40 45

Leu Val Arg Leu Arg Glu Arg Tyr Pro Trp Leu Val Ala Glu Val Asp
 50 55 60

Gly Glu Val Ala Gly Ile Ala Tyr Ala Gly Pro Trp Lys Ala Arg Asn
 65 70 75 80

Ala Tyr Asp Trp Thr Ala Glu Ser Thr Val Tyr Val Ser Pro Arg His
85 90 95

Gln Arg Thr Gly Leu Gly Ser Thr Leu Tyr Thr His Leu Leu Lys Ser
100 105 110

Leu Glu Ala Gln Gly Phe Lys Ser Val Val Ala Val Ile Gly Leu Pro
115 120 125

Asn Asp Pro Ser Val Arg Met His Glu Ala Leu Gly Tyr Ala Pro Arg
130 135 140

Gly Met Leu Arg Ala Ala Gly Phe Lys His Gly Asn Trp His Asp Val
145 150 155 160

Gly Phe Trp Gln Leu Asp Phe Ser Leu Pro Val Pro Pro Arg Pro Val
165 170 175

Leu Pro Val Thr Glu Ile
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Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile	100	105	110	
tgt act acg cag ctg cgc ctg ctc tcc tga				366
Cys Thr Thr Gln Leu Arg Leu Leu Ser	115	120		
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Met Gly Lys Gly Val Lys Ser Pro Gly Glu Lys Ser Arg Tyr Glu Thr	1	5	10	15
Ser Leu Asn Leu Thr Thr Lys Arg Phe Leu Glu Leu Leu Ser His Ser	20	25	30	
Ala Asp Gly Val Val Asp Leu Asn Trp Ala Ala Glu Val Leu Lys Val	35	40	45	
Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu Glu Gly Ile Gln	50	55	60	
Leu Ile Ala Lys Lys Ser Lys Asn His Ile Gln Trp Leu Gly Ser His	65	70	75	80
Thr Thr Val Gly Val Gly Gly Arg Leu Glu Gly Leu Thr Gln Asp Leu	85	90	95	
Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile	100	105	110	
Cys Thr Thr Gln Leu Arg Leu Leu Ser	115	120		